IN THE CLAIMS

Claims 20-22 and 24-26 are canceled herein without prejudice or disclaimer. Please note that all claims currently pending and under consideration in the referenced application are shown below. Please enter these claims as amended. This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS

1. (Previously presented) A primer specific and mispair extension assay for determining genotype, said assay comprising:

a) extending a nucleic acid sequence from a patient sample with *pfu* DNA polymerase, using a primer specific for a genotype to be determined, and

an incomplete set of dNTPs in the absence of ddNTPs, under suitable conditions for obtaining one or more extension products of the primer wherein said one or more extension products are terminated in the presence of at least two mispairs within a 2 to 4 base pair range located downstream of the 3' end of the primer; and wherein at least one of the primer or the dNTPs is labeled;

b) characterizing the extension products; and

c) analyzing the characterized extension products based on primer-specific pairing and non-specific pairing to determine the genotype of the nucleic acid sequence extended.

2. (Original) The assay according to claim 1, wherein the step of characterizing the extension products comprises the step of separating by size said extension products.

3. (Original) The assay according to claim 1, further comprising before step a) the step of amplifying the nucleic acid sequence.

4. (Original) The assay according to claim 3, wherein the incomplete set of dNTPs contains three different types of nucleotides.

5. (Original) The assay according to claim 4, wherein the incomplete set of dNTPs contains two different types of nucleotides.

6. (Original) The assay according to claim 5, wherein the primer is labeled with a radioactive label.

7. (Original) The assay according to claim 6, wherein one of the dNTPs is labeled with a radioactive label.

8. (Original) The assay according to claim 7, wherein the primer is labeled with a fluorescent label.

9. (Previously presented) The assay according to claim 1, wherein said extending, said characterizing and said analyzing are automated.

10. (Original) The assay according to claim 9, wherein the step of characterizing the extension products further comprises after the step of separating by size the extension products the step of sequencing the extension products.

11. (Original) The assay according to claim 2, further comprising sequencing the extension products after separating the extension products by size.

12. (Original) The assay according to claim 11, wherein said primer is selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 2, SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 13, SEQ ID NO. 14 and SEQ ID NO. 15.

13. (Canceled)

14. (Previously presented) The assay according to claim 23, wherein said genotype is determined based on an analysis of a genotype specific primer pairing and non-specific pairing.

15. (Previously presented) The assay according to claim 23, wherein said analysis is based on the termination of primer extension by mispair(s) and on primer specific pairing and non-specific pairing extension on a template.

16. (Canceled)

17. (Previously presented) The primer specific and mispair extension assay of claim 1 wherein said at least two mispairs are created immediately following one correct pairing at the position immediately adjacent to said 3' end of the primer.

18. (Previously presented) The primer specific and mispair extension assay of claim 1 wherein said at least two mispairs are separated by one or two correct pairings.

19. (Previously presented) The primer specific and mispair extension assay of claim 1 wherein said at least two mispairs are consecutive mispairs.

20. (Canceled)

21. (Canceled)

22. (Canceled)

23. (Previously presented) A primer specific and mispair extension assay for determining genotype, said assay comprising:

a) extending a nucleic acid sequence from a patient sample with *pfu* DNA polymerase, using a primer specific for a genotype to be determined, and an incomplete set of dNTPs in the absence of ddNTPs, under suitable conditions for obtaining extension products of the primer based on specific pairing and non-specific pairing, wherein said extension products are terminated in the presence of at least two mispairs within a 2 to 4 base pair range located downstream of the 3' end of the primer, and wherein at least one of the primer or dNTPs is labeled;

b) separating the extension products obtained;

c) characterizing the extension products;

d) generating a genotype-specific extension profile of the extension products; and

e) analyzing the genotype-specific extension profiles to determine a genotype of the nucleic acid sequence.

24. (Canceled)

25. (Canceled)

26. (Canceled)

IN THE DRAWINGS

The attached annotated sheet of drawings includes proposed changes to FIG. 1. FIG. 1 has been amended to include both the original SEQ ID NO. references noted in the originally filed figure, and the corresponding column references (II-1, II-2, II-3 and II-4) as amended in the Response dated October 28, 2003. Also attached is a replacement sheet including FIG. 1 with the proposed changes and which replaces the original sheet including FIG. 1.